

F-Harnuel

1646

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/037,657A

DATE: 09/03/1999
TIME: 14:40:16

Input Set: I037657A.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

1 <110> APPLICANT: Hilton, Douglas J.
2 Nicola, Nicos A.
3 Farley, Alison
4 Wilson, Tracy
5 Zhang, Jian-Guo
6 Alexander, Warren
7 Rakar, Steven
8 Fabri, Louis
9 Kojima, Tetsuo
10 Maeda, Masatsugu
11 Kikuchi, Yasufumi
12 Nash, Andrew
13 <120> TITLE OF INVENTION: A NOVEL HAEMPOIETIN RECEPTOR AND GENETIC SEQUENCES
14 ENCODING SAME
15 <130> FILE REFERENCE: DAVIES COLLISON CAVE (CIP)
16 <140> CURRENT APPLICATION NUMBER: US/09/037,657A
17 <141> CURRENT FILING DATE: 1998-03-10
18 <150> EARLIER APPLICATION NUMBER: 08/928,720
19 <151> EARLIER FILING DATE: 1997-09-11
20 <160> NUMBER OF SEQ ID NOS: 54
21 <170> SOFTWARE: PatentIn Ver. 2.0
22 <210> SEQ ID NO 1
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25 <213> ORGANISM: Unknown
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Description of Unknown Organism: haemopoietin receptor
28 <220> FEATURE:
29 <221> NAME/KEY: UNSURE
30 <222> LOCATION: (3)
31 <223> OTHER INFORMATION: Unsure at position 3
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34 1 5
35 <210> SEQ ID NO 2
36 <211> LENGTH: 24
37 <212> TYPE: DNA
38 <213> ORGANISM: Artificial Sequence
39 <220> FEATURE:
40 <223> OTHER INFORMATION: Description of Artificial Sequence: M116 probe
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43 <210> SEQ ID NO 3
44 <211> LENGTH: 24

ENTERED

seq. 5

w-->α

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45 <212> TYPE: DNA
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53 <212> TYPE: DNA
54 <213> ORGANISM: Artificial Sequence
55 <220> FEATURE:
56 <223> OTHER INFORMATION: Description of Artificial Sequence:M159 probe
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60 <211> LENGTH: 24
61 <212> TYPE: DNA
62 <213> ORGANISM: Artificial Sequence
63 <220> FEATURE:
64 <223> OTHER INFORMATION: Description of Artificial Sequence:M242 probe
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67 <210> SEQ ID NO 6
68 <211> LENGTH: 22
69 <212> TYPE: DNA
70 <213> ORGANISM: Artificial Sequence
71 <220> FEATURE:
72 <223> OTHER INFORMATION: Description of Artificial Sequence:M112 probe
73 <400> SEQUENCE: 6
74      agctgctgtt aaagggttc tc                    22
75 <210> SEQ ID NO 7
76 <211> LENGTH: 15
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83 <222> LOCATION: (1)
84 <223> OTHER INFORMATION: Unsure at position 1
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91 <222> LOCATION: (10)
92 <223> OTHER INFORMATION: Unsure at position 10
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94      rctccartcr ctcca                15

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102 <221> NAME/KEY: unsure
103 <222> LOCATION: (1)
104 <223> OTHER INFORMATION: Unsure at position 1
105 <220> FEATURE:
106 <221> NAME/KEY: unsure
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108 <223> OTHER INFORMATION: Unsure at position 7
109 <220> FEATURE:
110 <221> NAME/KEY: unsure
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112 <223> OTHER INFORMATION: Unsure at position 10
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114      rctccaytcr ctcca                                15
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117 <212> TYPE: DNA
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119 <220> FEATURE:
120 <223> OTHER INFORMATION: Description of Artificial Sequence:1944 probe
121 <400> SEQUENCE: 9
122      aagtgtgacc atcatgtgga c                                21
123 <210> SEQ ID NO 10
124 <211> LENGTH: 18
125 <212> TYPE: DNA
126 <213> ORGANISM: Artificial Sequence
127 <220> FEATURE:
128 <223> OTHER INFORMATION: Description of Artificial Sequence:2106 probe
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132 <211> LENGTH: 18
133 <212> TYPE: DNA
134 <213> ORGANISM: Artificial Sequence
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Description of Artificial Sequence:2120 probe
137 <400> SEQUENCE: 11
138      atgcccgcgg gtcgcccg                                18
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140 <211> LENGTH: 1629
141 <212> TYPE: DNA
142 <213> ORGANISM: Unknown
143 <220> FEATURE:
144 <221> NAME/KEY: CDS

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145 <222> LOCATION: (124)..(1362)
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147 <223> OTHER INFORMATION: Description of Unknown Organism: Murine NR6.1
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150 ccccgagac tgcggccgc gccataccgg cggtgcagtc accgcccgtt gcgcgccacc 120
151 ccc atg ccc gcg ggt cgc ccg ggc ccc gtc gcc caa tcc gcg cgg cgg 168
152 Met Pro Ala Gly Arg Pro Gly Pro Val Ala Gln Ser Ala Arg Arg
153 1 5 10 15
154 ccg ccg cgg ccg ctg tcc tgc ctg tgg tgc cct ctg ttg ctc tgt gtc 216
155 Pro Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val
156 20 25 30
157 ctc ggg gtg cct cgg ggc gga tgc gga gcc cac aca gct gta atc agc 264
158 Leu Gly Val Pro Arg Gly Gly Ser Gly Ala His Thr Ala Val Ile Ser
159 35 40 45
160 ccc cag gac ccc acc ctt ctc atc ggc tcc tcc ctg caa gct acc tgc 312
161 Pro Gln Asp Pro Thr Leu Leu Ile Gly Ser Ser Leu Gln Ala Thr Cys
162 50 55 60
163 tct ata cat gga gac aca cct ggg gcc acc gct gag ggg ctc tac tgg 360
164 Ser Ile His Gly Asp Thr Pro Gly Ala Thr Ala Glu Gly Leu Tyr Trp
165 65 70 75
166 acc ctc aat ggt cgc cgc ctg ccc tct gag ctg tcc cgc ctc ctt aac 408
167 Thr Leu Asn Gly Arg Arg Leu Pro Ser Glu Leu Ser Arg Leu Leu Asn
168 80 85 90 95
169 acc tcc acc ctg gcc ctg gcc ctg gct aac ctt aat ggg tcc agg cag 456
170 Thr Ser Thr Leu Ala Leu Ala Leu Ala Asn Leu Asn Gly Ser Arg Gln
171 100 105 110
172 cag tca gga gac aat ctg gtg tgt cac gcc cga gac ggc agc att ctg 504
173 Gln Ser Gly Asp Asn Leu Val Cys His Ala Arg Asp Gly Ser Ile Leu
174 115 120 125
175 gct ggc tcc tgc ctc tat gtt ggc ttg ccc cct gag aag ccc ttt aac 552
176 Ala Gly Ser Cys Leu Tyr Val Gly Leu Pro Pro Glu Lys Pro Phe Asn
177 130 135 140
178 atc agc tgc tgg tcc cgg aac atg aag gat ctc acg tgc cgc tgg aca 600
179 Ile Ser Cys Trp Ser Arg Asn Met Lys Asp Leu Thr Cys Arg Trp Thr
180 145 150 155
181 ccg ggt gca cac ggg gag aca ttc tta cat acc aac tac tcc ctc aag 648
182 Pro Gly Ala His Gly Glu Thr Phe Leu His Thr Asn Tyr Ser Leu Lys
183 160 165 170 175
184 tac aag ctg agg tgg tac ggt cag gat aac aca tgt gag gag tac cac 696
185 Tyr Lys Leu Arg Trp Tyr Gly Gln Asp Asn Thr Cys Glu Glu Tyr His
186 180 185 190
187 act gtg ggc cct cac tca tgc cat atc ccc aag gac ctg gcc ctc ttc 744
188 Thr Val Gly Pro His Ser Cys His Ile Pro Lys Asp Leu Ala Leu Phe
189 195 200 205
190 act ccc tat gag atc tgg gtg gaa gcc acc aat cgc cta ggc tca gca 792
191 Thr Pro Tyr Glu Ile Trp Val Glu Ala Thr Asn Arg Leu Gly Ser Ala
192 210 215 220
193 aga tct gat gtc ctc aca ctg gat gtc ctg gac gtg gtg acc acg gac 840
194 Arg Ser Asp Val Leu Thr Leu Asp Val Leu Asp Val Val Thr Thr Asp

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195          225          230          235
196    ccc cca ccc gac gtg cac gtg agc cgc gtt ggg ggc ctg gag gac cag 888
197    Pro Pro Pro Asp Val His Val Ser Arg Val Gly Gly Leu Glu Asp Gln
198    240          245          250          255
199    ctg agt gtg cgc tgg gtc tca cca cca gct ctc aag gat ttc ctc ttc 936
200    Leu Ser Val Arg Trp Val Ser Pro Pro Ala Leu Lys Asp Phe Leu Phe
201          260          265          270
202    caa gcc aag tac cag atc cgc tac cgc gtg gag gac agc gtg gac tgg 984
203    Gln Ala Lys Tyr Gln Ile Arg Tyr Arg Val Glu Asp Ser Val Asp Trp
204          275          280          285
205    aag gtg gtg gat gac gtc agc aac cag acc tcc tgc cgt ctc gcg ggc 1032
206    Lys Val Val Asp Asp Val Ser Asn Gln Thr Ser Cys Arg Leu Ala Gly
207          290          295          300
208    ctg aag ccc ggc acc gtt tac ttc gtc caa gtg cgt tgt aac cca ttc 1080
209    Leu Lys Pro Gly Thr Val Tyr Phe Val Gln Val Arg Cys Asn Pro Phe
210          305          310          315
211    ggg atc tat ggg tgc aaa aag gcg gga atc tgg agc gag tgg agc cac 1128
212    Gly Ile Tyr Gly Ser Lys Lys Ala Gly Ile Trp Ser Glu Trp Ser His
213    320          325          330          335
214    ccc acc gct gcc tcc acc cct cga agt gag cgc ccg ggc ccg ggc ggc 1176
215    Pro Thr Ala Ala Ser Thr Pro Arg Ser Glu Arg Pro Gly Pro Gly Gly
216          340          345          350
217    ggg gtg tgc gag ccg cgg ggc ggc gag ccc agc tgc ggc ccg gtg cgg 1224
218    Gly Val Cys Glu Pro Arg Gly Gly Glu Pro Ser Ser Gly Pro Val Arg
219          355          360          365
220    cgc gag ctc aag cag ttc ctc ggc tgg ctc aag aag cac gca tac tgc 1272
221    Arg Glu Leu Lys Gln Phe Leu Gly Trp Leu Lys Lys His Ala Tyr Cys
222          370          375          380
223    tgc aac ctt agt ttc cgc ctg tac gac cag tgg cgt gct tgg atg cag 1320
224    Ser Asn Leu Ser Phe Arg Leu Tyr Asp Gln Trp Arg Ala Trp Met Gln
225          385          390          395
226    aag tca cac aag acc cga aac cag gtc ctg ccg gct aaa ctc 1362
227    Lys Ser His Lys Thr Arg Asn Gln Val Leu Pro Ala Lys Leu
228    400          405          410
229    taaggatagg ccacccctct gctgggtcag acctggaggc tcacctgaat tggagcccct 1422
230    ctgtaccatc tgggcaacaa agaaacctac cagaggctgg ggcacaatga gctcccacaa 1482
231    ccacagcttt ggtccacatg atggtcacac ttggatatac cccagtgtgg gtaaggttgg 1542
232    ggtattgcag ggccctccaa caatctcttt aaataaataa aggagttgtt caggtaaaaa 1602
233    aaaaaaaaaa aaaaaaaaaa aaaaaaa 1629
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235    <211> LENGTH: 413
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237    <213> ORGANISM: Unknown
238    <220> FEATURE:
239    <223> OTHER INFORMATION: Description of Unknown Organism: Murine NR6.1
240    <400> SEQUENCE: 13
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242    1          5          10          15
243    Pro Arg Pro Leu Ser Ser Leu Trp Ser Pro Leu Leu Leu Cys Val Leu
244          20          25          30

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I037657A.RAW

Line	?	Error/Warning	Original Text
33	W	"N" or "Xaa" used: Feature required	Trp Ser Xaa Trp Ser
1032	W	"N" or "Xaa" used: Feature required	Leu Arg Leu Val Arg Ser Glu Xaa His Met X
1036	W	"N" or "Xaa" used: Feature required	Leu Xaa Asp Leu Gly Gly Ser His Gln Ser P
1038	W	"N" or "Xaa" used: Feature required	Xaa Cys Pro His Thr Gly Cys Pro Gly Arg